

Reviewer Report

Title: rnaSPAdes: a de novo transcriptome assembler and its application to RNA-Seq data

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Reviewer name: Zhong Wang

Reviewer Comments to Author:

General comments:

Drawing a close analogy between single-cell genome assembly and transcriptome assembly, Bushmanova et al developed rnaSPAdes for de novo transcriptome assembly. The authors benchmarked their software on several synthetic and real-world datasets. They also compared the performance of rnaSPAdes with a few alternative assemblers by measuring several independent metrics. Based on these results, the authors conclude that rnaSPAdes is a "decent" transcriptome assembler, as it offers very good sensitivity, good specificity, and good computing efficiency. The analyses presented in this work are comprehensive, and their conclusion is sufficiently supported by the presented evidence. The paper is well written and easy to follow.

I have the following specific comments for minor revision:

- 1) Figure 3, the bars for Z. mayes are rather low. It should help reads to make a better comparison by using a different vertical scale than the rest, as the absolute total number of genes assembled here are not important.
- 2) The specific version numbers for each software tools should be noted
- 3) This could be optional: some further discussion of the misassemblies could be very informative. For example, one of these reasons may lead to misassemblies: a) paralogous genes b) complex splicing, or genes with many exons/isoforms c) Merge of overlapping genes because of non-strand-specific data is used

Level of Interest

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